CCH1A4 FINAL PROJECT 2019/2020

Submitted by email to jimmytirtawangsa@telkomuniversity.ac.id
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In this final project will simulate how a virus spread and whether it is possible to die down. The simulation space is very simple, it will be an **n×m** matrix. Each cell of the matrix will represent population in an area, such as a housing complex, an apartment building, etc. Figure 1 shows the matrix, which each cell populated by **p** people.

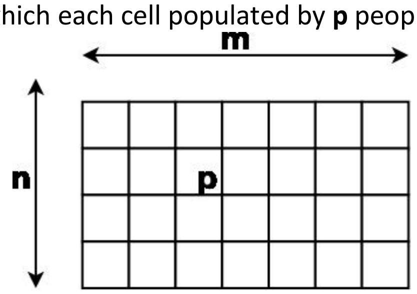

Fig. 1. n×m region, each cell is populated by p people.

The area will connect to the surrounding neighborhoods; left, right, top, down, top-left, top-right, bottom-left, and bottom-right neigbors as shown in figure 2. Of course cells on the sides and the corners will have fewer neighbors.

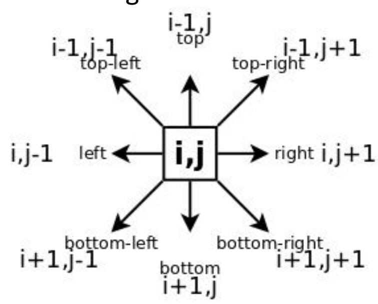

Fig. 2. Various neighbors (x,y) of cell (i,j)

Some people in the cell, who already have the virus, may infect other within the cell and spread the virus to other neighboring cells.
It is important to detect who have the virus and treat them, so they will not spread the virus to others.
There are two possible outcomes after hospitalized; either they can become healthy again or they die.

The following are information stored in each cell (i,j):

1. The number of population (living people) in the cell $p_{i,j}$ are people live in the cell, either healthy or have yet undetected viruses ($c_{i,j}$). People who are hospitalized or who already died are excluded from $p_{i,j}$.
2. The number of infected (yet undetected) people $c_{i,j}$. Obviously then at any time $c_{i,j} \leq p_{i,j}$
3. The number of hospitalized (i.e. detected) people $h_{i,j}$. Hospitalized people should be discounted from, i.e. not counted as part of, the population

Some global parameters are:

1. Rate of infection within a cell **rate1** people infected per time per already infected person.
2. Rate of infection to neighboring cells: **rate2** people per time per already infected person
3. Rate of detected people; **rate3** people per time per already infected person

4. Rate of recovering people; **rate4** people per time per hospitalized person
5. Rate of dying people; **rate5** people per time per hospitalized person

The rules of infections are as follows (all at simulation time t):

1. If in a cell (i,j) there is $c_{i,j}$ undetected infected people, then on time t+1 there will be $c_{i,j}\times$rate1 people infected in the cell.
2. If in a cell (i,j) there is $c_{i,j}$ undetected infected people infected, then on time t+1 at the neighbor cell (x,y) there will be $c_{i,j}\times$rate2$\times p_{x,y}+c_{x,y}$ indetected infected people.
3. If in a cell (i,j) there is $c_{i,j}$ undetected infected people, then on time t+1 there will be $c_{i,j}\times$rate3 + $h_{i,j}$ hospitalized people.
4. If in a cell (i,j) there is $h_{i,j}$ hospitalized people, then on time t+1 there will be $h_{i,j}\times$rate4 who are recovered and going back to the population, i.e. added back to $p_{i,j}$
5. If in a cell (i,j) there is $h_{i,j}$ hospitalized people, then on time t+1 there will be $h_{i,j}\times$rate5 who will die

Based on this community structure, global parameters, and infection rules, you should create a program that simulate the spread of the virus. Later from a given set of parameters (the rates, initial values of $p_{i,j}$ and $c_{i,j}$) your program could determine whether the virus will wipe out all the population, the people will recover, or the virus will stay infected the community for a long time.

After given t time, your program should terminate and give the following information:

1. Original total of size of population
2. The total people hospitalized during simulation
3. The total people died during simulation
4. The highest increase of infection during simulation
5. The start of reduction of the number of infected people